Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:37:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068143.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6068143 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068143.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:37:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,594,241
Mapped reads	4,359,726 / 94.9%
Unmapped reads	234,515 / 5.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,800 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	463,807 / 10.1%
Duplication rate	8.71%
Clipped reads	2,268,444 / 49.38%

2.2. ACGT Content

Number/percentage of A's	75,401,822 / 26.71%
Number/percentage of C's	50,724,855 / 17.97%
Number/percentage of T's	91,800,187 / 32.51%
Number/percentage of G's	64,384,079 / 22.8%
Number/percentage of N's	32,528 / 0.01%
GC Percentage	40.77%

2.3. Coverage

Mean	0.0912

Standard Deviation	0.8937

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

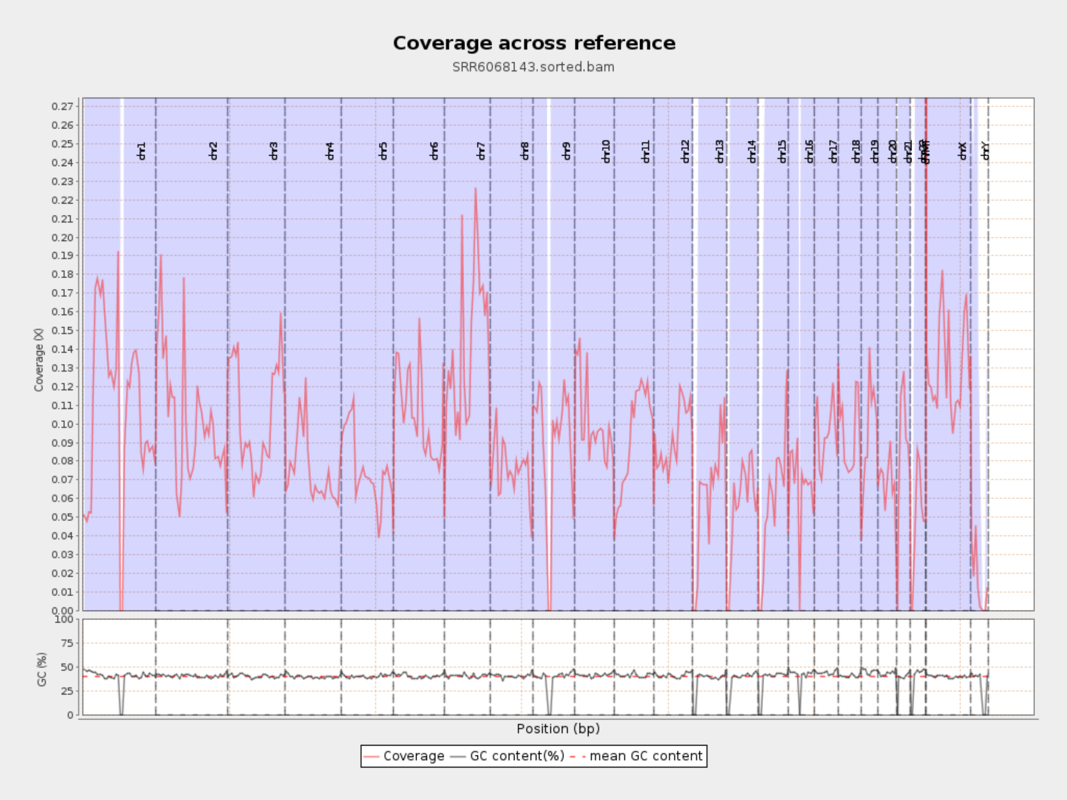
General error rate	0.6%
Mismatches	1,667,466
Insertions	18,363
Mapped reads with at least one insertion	0.42%
Deletions	71,520
Mapped reads with at least one deletion	1.62%
Homopolymer indels	45.77%

2.6. Chromosome stats

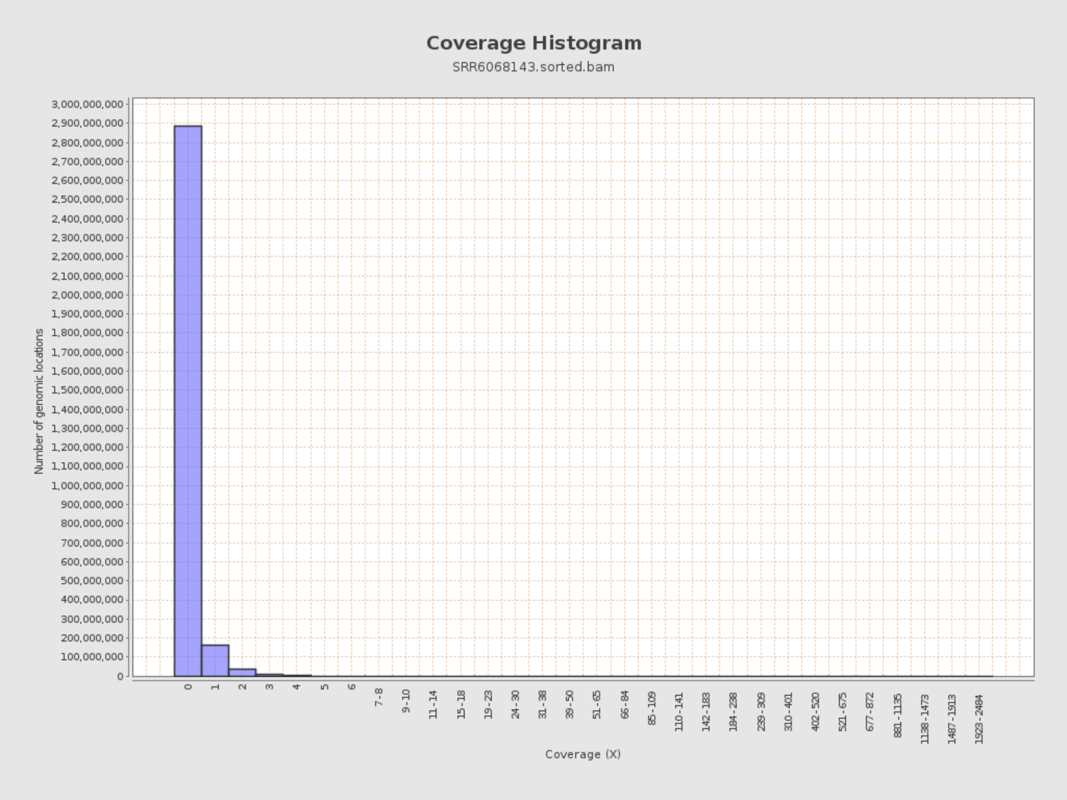
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27091493	0.1087	2.0243
chr2	243199373	25139734	0.1034	0.9451
chr3	198022430	20849494	0.1053	0.4166
chr4	191154276	14419821	0.0754	0.4137
chr5	180915260	13676281	0.0756	0.3604
chr6	171115067	18156271	0.1061	0.5229
chr7	159138663	22551658	0.1417	1.4483

chr8	146364022	11004752	0.0752	1.2253
chr9	141213431	12483193	0.0884	0.6718
chr10	135534747	13740894	0.1014	0.6369
chr11	135006516	12596705	0.0933	0.5693
chr12	133851895	12416590	0.0928	0.4302
chr13	115169878	7303312	0.0634	0.3331
chr14	107349540	6080768	0.0566	0.3905
chr15	102531392	5908698	0.0576	0.348
chr16	90354753	5892502	0.0652	0.3853
chr17	81195210	7821059	0.0963	0.4459
chr18	78077248	7411856	0.0949	1.1715
chr19	59128983	5678169	0.096	1.256
chr20	63025520	4355482	0.0691	0.3796
chr21	48129895	4089181	0.085	0.4128
chr22	51304566	2430702	0.0474	0.2748
chrMT	16571	273588	16.51	10.1513
chrX	155270560	20205888	0.1301	0.5496
chrY	59373566	892618	0.015	0.3663

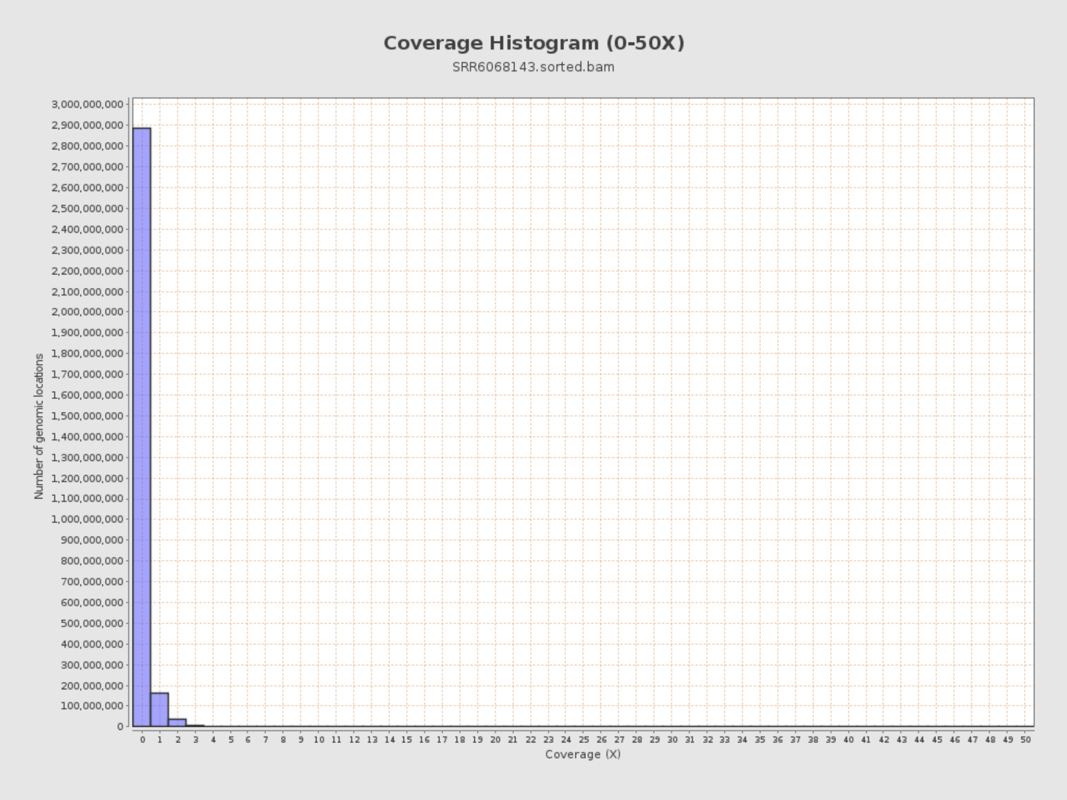
3. Results : Coverage across reference



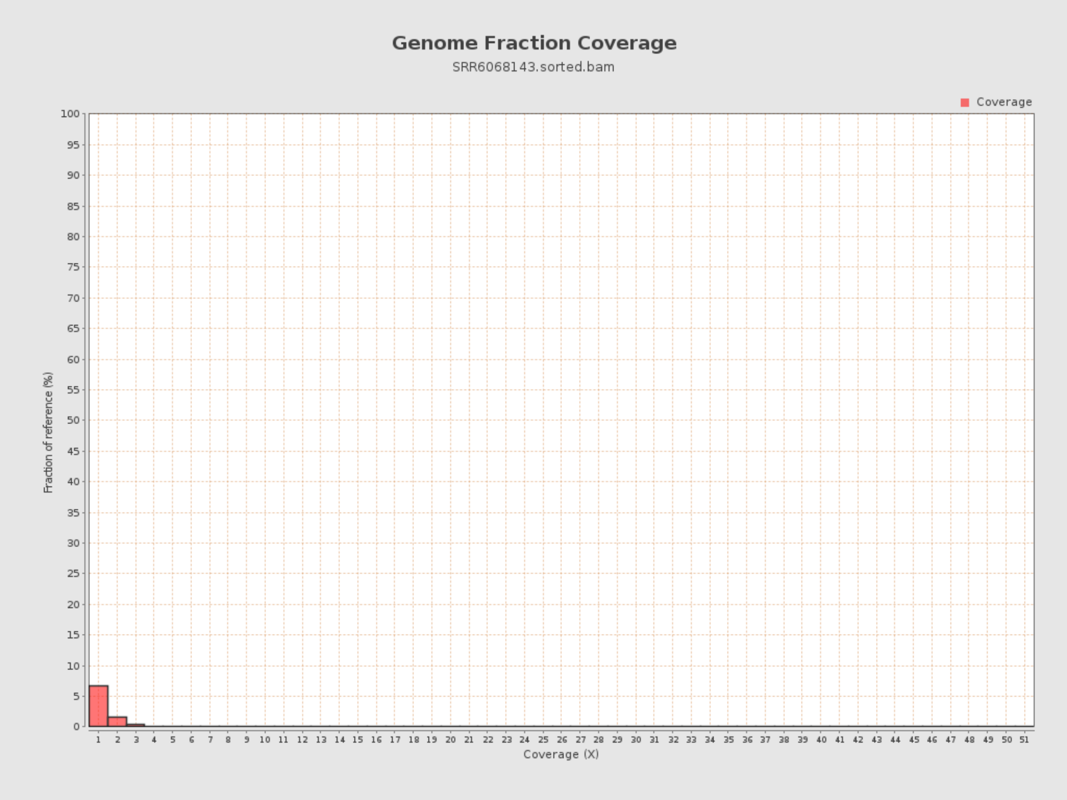
4. Results : Coverage Histogram



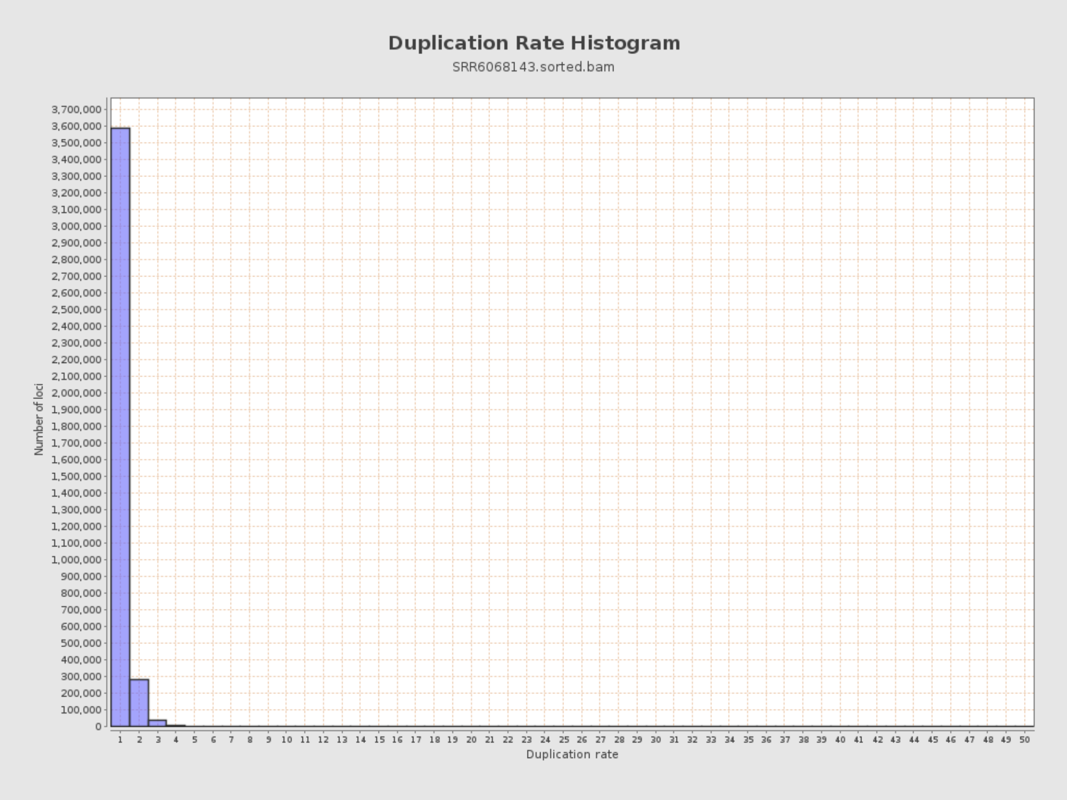
5. Results : Coverage Histogram (0-50X)



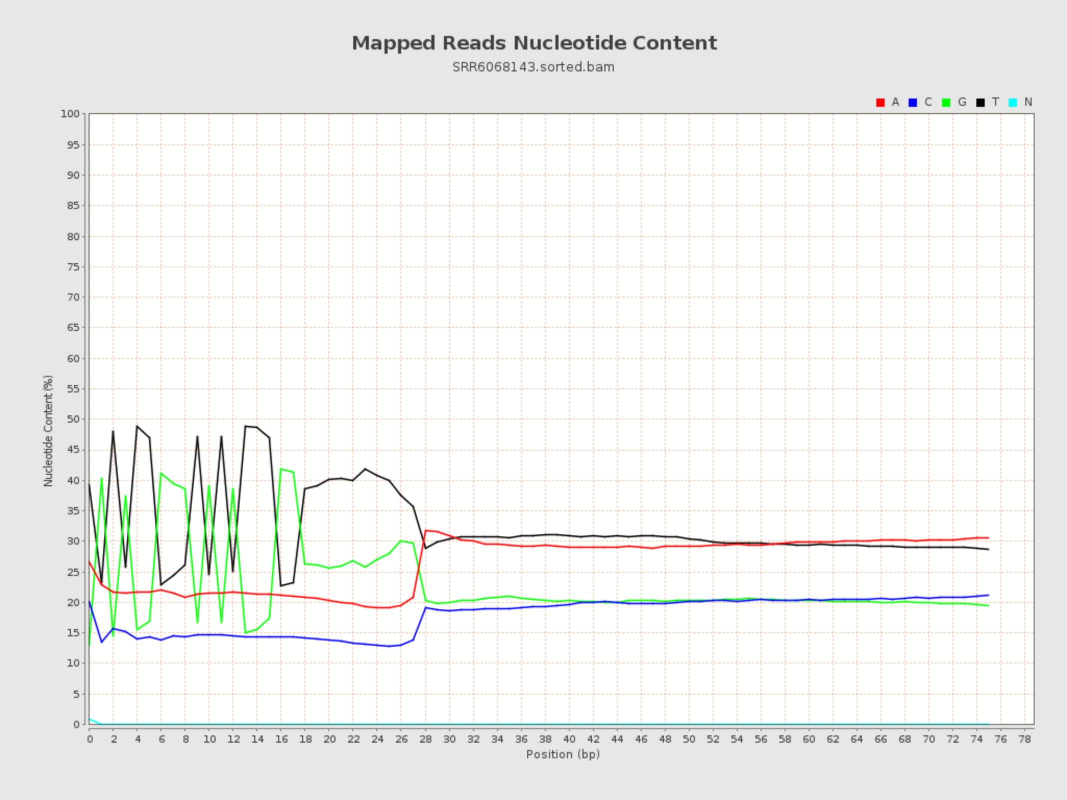
6. Results : Genome Fraction Coverage



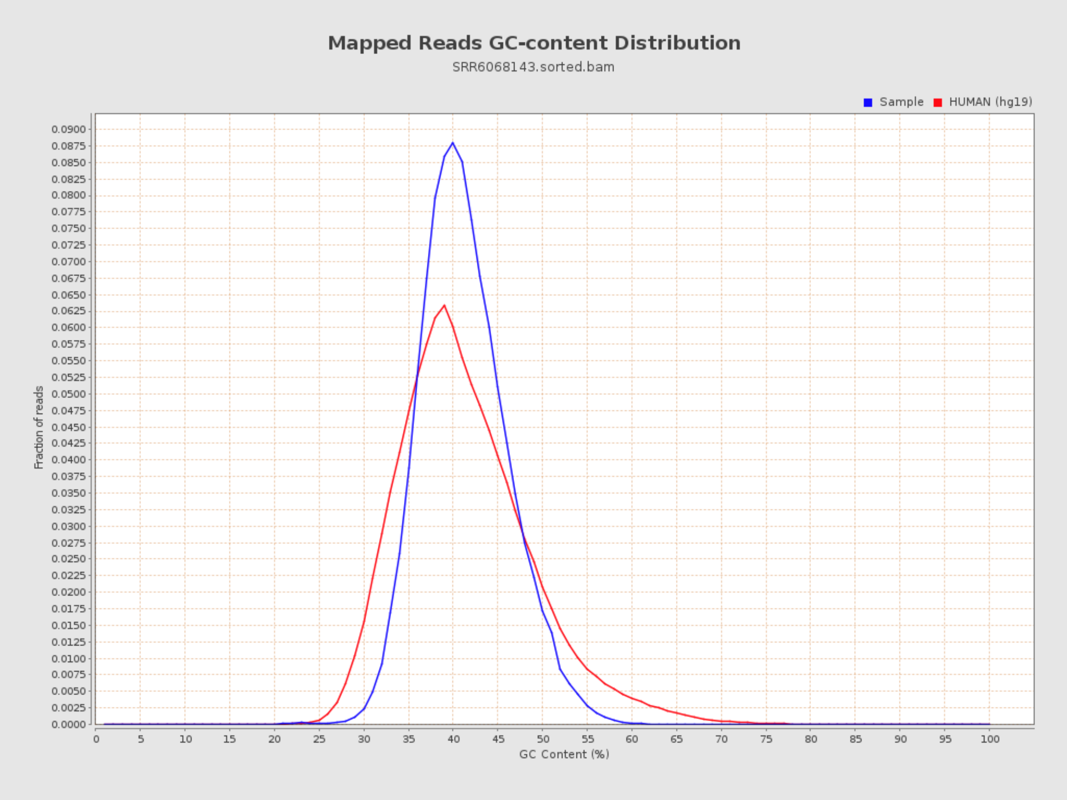
7. Results : Duplication Rate Histogram



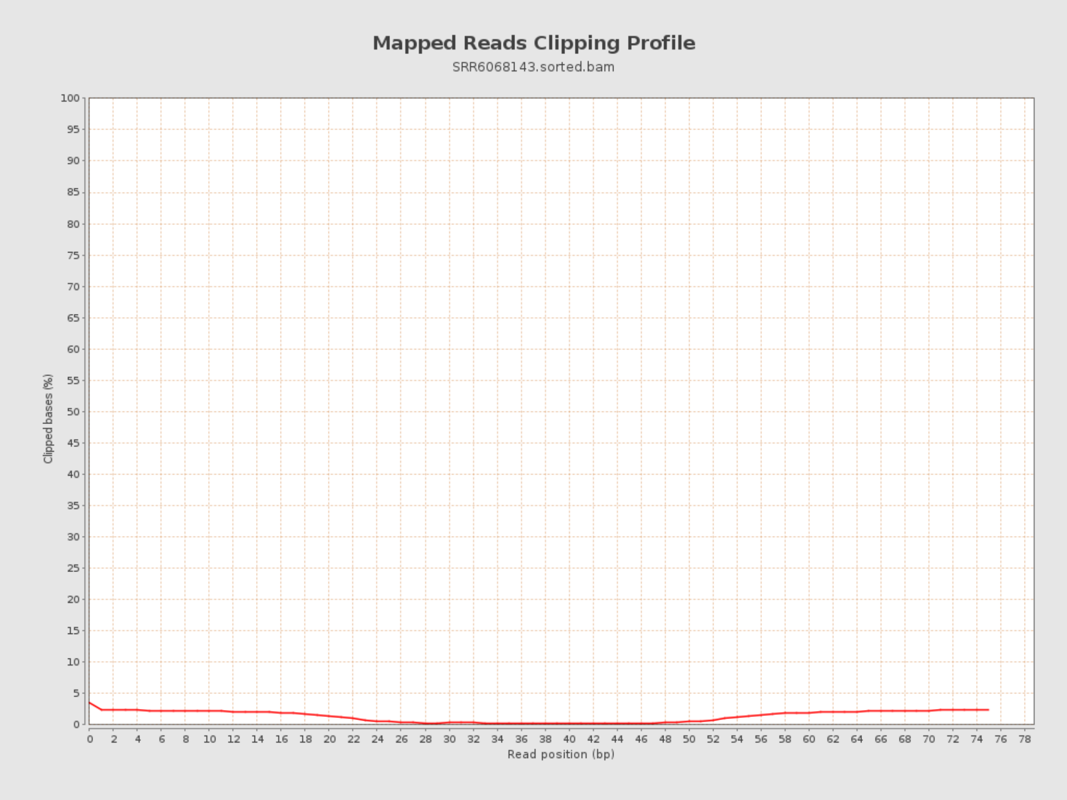
8. Results : Mapped Reads Nucleotide Content



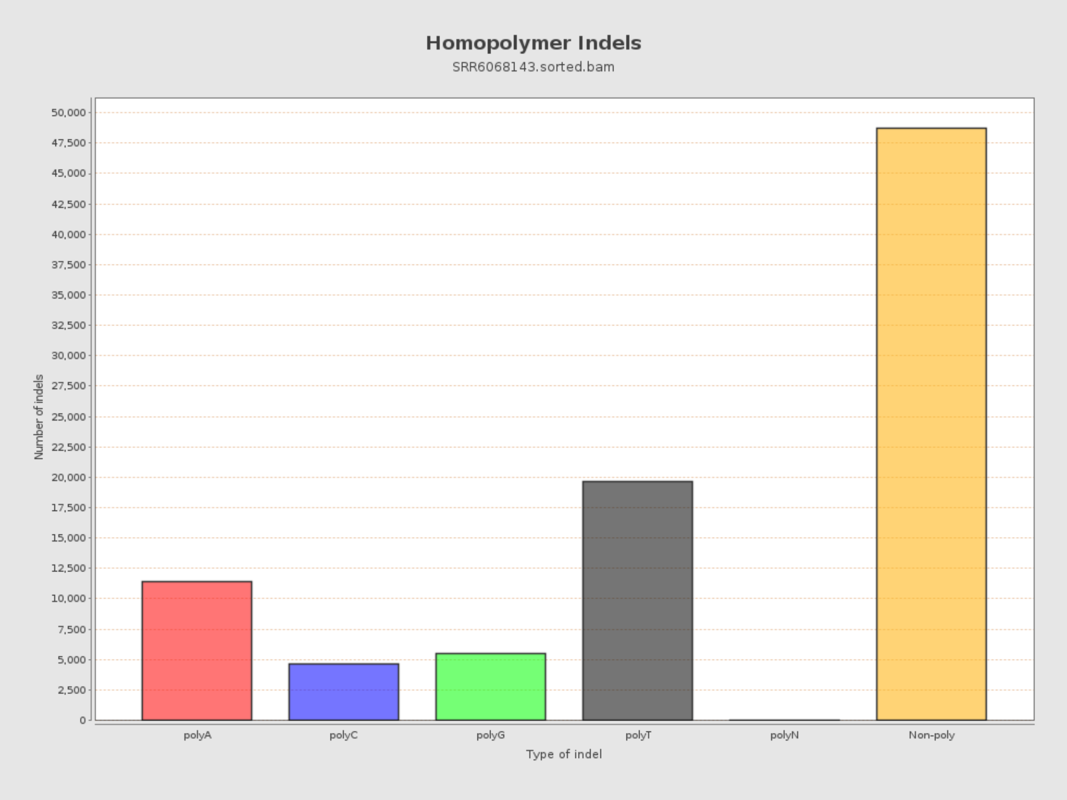
9. Results : Mapped Reads GC-content Distribution



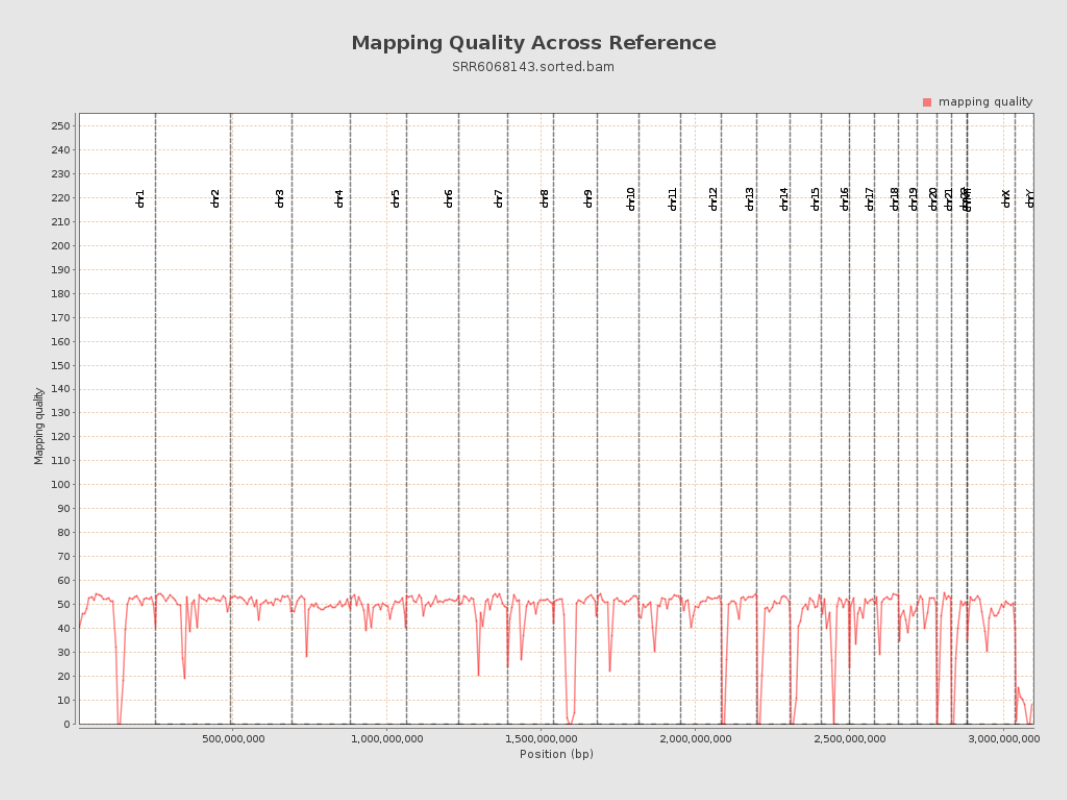
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram